



SEQ ID NO:90

3684 nucleotides

DNA

Arabidopsis thaliana

CDS

(501)..(557)

(689)..(818)

(1008)..(1114)

(1194)..(1320)

(1469)..(1576)

(1671)..(1786)

(1858)..(1941)

(2040)..(2108)

(2198)..(2269)

(2352)..(2443)

(2545)..(2672)

(2772)..(2873)

(2965)..(3032)

(3122)..(3181)

agcgattcct tagcagaaag gcgttccatt tctctggcgt aaaccaaagg agatccttga 60

actgtttcct gcaccattgc tctaaaacc cttctccggc acgaattttt ccaaccctgc 120

ttcaccaccg gaacattgag acaaaatctc gacggtgacg ctgagggtga aaaaaccaat 180

cgaaccgcag acgtaccagg aaccgaacca tgttatcaacg ccattgaaga agaagaagaa 240

gaagaaggta aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga 300

*FIG. 19A*

aaaaagagtt aaggtagggag tgtctggttc aaccgggtta tatccggttc aaattaaacc	360
tcttacagtt aaccgggttt tgggttttgt tcgattgttc ataaaagaaa gaagacttt	420
gtcgatcgatt agtgccaaag ttgaaagttt aacaccttgc tcagaatttt ctgctcgtt	480
ctgagttttt tttcccgcc atg gaa atc gac tcc gag aaa att cac gaa agg Met Glu Ile Asp Ser Glu Lys Ile His Glu Arg	533
1 5 10	
aag caa tcc gat tac aat tcg ctg gtacgaactc tattacttta tcgacttgc Lys Gln Ser Asp Tyr Asn Ser Leu	587
15	
gtgaaagaca aatgtaatca ttctgtgtgg tgactgtttc tacttataag tgtacggct	647
agggtttgtt atctgattct gagttttgc aattgaagca g gat gag aga ttc gag Asp Glu Arg Phe Glu	703
20	
ata cag aag gag atg tac aga ggt cag caa tac agt cag att tac ttt Ile Gln Lys Glu Met Tyr Arg Gly Gln Gln Tyr Ser Gln Ile Tyr Phe	751
25 30 35 40	
gct cgt ctt cat ctc atg aga aca ctt ctc tac tct ctt gct cct act Ala Arg Leu His Leu Met Arg Thr Leu Leu Tyr Ser Leu Ala Pro Thr	799
45 50 55	
tgg aaa tct cat ttg cct g gtcagtgcgtt ttgtttctct catatttgc Trp Lys Ser His Leu Pro	848
60	
acaacaacga agagcagttt ttgagaattt tcttgggtta gatataattt ggtgaaatca	908
gtgattttta gggatttttg ctatcttatg gattacagtt gagaaagatt gctgtatttgc	968
tttaaattat agatctgaat gtgaatttca ttttgcag tg tgt aag gtt ttg Val Cys Lys Val Leu	1021
65	
gga ctt gaa aaa gga aaa gaa tgc ata att gtg gga acc ttg ttc aaa Gly Leu Glu Lys Gly Lys Glu Cys Ile Ile Val Gly Thr Leu Phe Lys	1069
70 75 80	

*FIG. 19B*

cac atg aag ctt aaa cct tgt gtt ctc gat gaa tat tct aaa gag His Met Lys Leu Lys Pro Cys Val Leu Asp Glu Tyr Ser Lys Glu 85 90 95	1114
gttggttttt attaacctct actgttttt tgagctatgt ctatgctgaa tcaatctgag tatatttaac ataatgcag agg tca gtt act ccg ctt gtt aaa cca cat aac Arg Ser Val Thr Pro Leu Val Lys Pro His Asn 100 105	1174 1226
ttt atg cat cct gat gat aat ctg atc ctc gaa gac gag agt ggg aga Phe Met His Pro Asp Asp Asn Leu Ile Leu Glu Asp Glu Ser Gly Arg 110 115 120 125	1274
gtt aag ctt gct ggt tcc gca ctt tca cct gcg att tat gtg aca g Val Lys Leu Ala Gly Ser Ala Leu Ser Pro Ala Ile Tyr Val Thr 130 135 140	1320
gtattgcaaa tgggttctta ctgttttac tgtatgattt ttcccttctt tacaatgtgg caaatcttag agattttgat caagcttcc tctctaaaaa gatgggttct ttaagaaaat	1380 1440
taacgttcaa gcctcccgta cattgttag gt gtt gtt gca ctg cat ggg Gly Val Val Val Ala Leu His Gly 145	1491
aag gaa act aat gct ggt gaa ttc ttt gtt gag gat gta cta gaa gct Lys Glu Thr Asn Ala Gly Glu Phe Phe Val Glu Asp Val Leu Glu Ala 150 155 160	1539
ggt tta cca cct cag att gag cggtt atc gat cta c gtaagtcttag Gly Leu Pro Pro Gln Ile Glu Arg Pro Ile Asp Leu 165 170 175	1586
ctatgttctc ttccctttgc taacctcatg gctcaatcat ttctataaggc aatctctcat	1646
gatacatcca tattgcatct gcag ag gaa gat aaa tat gtc gtg tta ttg Gln Glu Asp Lys Tyr Val Val Leu Leu 180 185	1696
tcg ggc ctt tgt att gga agc aaa tcg gct aat ccc ctg cag ttt cag Ser Gly Leu Cys Ile Gly Ser Lys Ser Ala Asn Pro Leu Gln Phe Gln 190 195 200	1744

*FIG. 19C*

ctt ctt gtt gac cat ata act ggg cat ctc gga gat gag gag Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu 205                    210                    215	1786
gttcaaatct cttaacttgc agttgttca acatatttct ttccttaatt tatactttat gaa caa ggc ctt gca gca cag ata gtt cat gta gta att Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile 220                    225	1846
gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln 230                    235                    240	1941
gtacttataa ctttgttgc tgatatattc tcagatacag ttccagtaat tatctgcccc atgtatgtct tatgatcttt attgggtgat ctttgtag aac ttg gcc tcg aaa gat Asn Leu Ala Ser Lys Asp 245	2001
caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Met Leu Ser 250                    255                    260                    265	2105
cag gtcagttAAC tggatctACG tgtgtgttAT cgatatCTAT tgAGATgAAA Gln	2158
gttcaactc ctgtttttt ttttgtggat tgtttttag ata gct gca gga gtt Ile Ala Ala Gly Val 270	2212
tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu 275                    280                    285	2260
cct cag cag gtctgcaaAT acataAGAAA cattcaAAAT cccgcATTt Pro Gln Gln 290	2309
gtatcgataa ctctgattca taggccttc tctttgttc ag cct ctg aat aga Pro Leu Asn Arg	2363

*FIG. 19D*

tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr 295               300               305               310	2411
aat cct cac tca ttt gat gtc gat aat atc ag gtatgattat tattaatagt Asn Pro His Ser Phe Asp Val Asp Asn Ile Arg 315               320	2463
tgaataacaat ctctctgatt ttacaacgat aaaattcttg ggtttatctg actgaaaacc	2523
tcatatgggg gcatttgca g a ttt ctt gga act tct ggt cag aac atc gat Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp 325               330	2575
gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu 335               340               345	2623
aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu 350               355               360	2672
gtaagaattc tccttgcctt gcaagattac tttttgaac taagccata aaaaaatgat	2732
ccttgagtt ctattggtt ttgattcaact tgcgtagacag gt tgt tat cct ttc Gly Cys Tyr Pro Phe 365	2785
acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe 370               375               380	2833
gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys 385               390               395	2883
cttacacaga gattagaaat aacattctct tttgtcaaac atcaggctt aactttctt	2943
gggttaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cggtt atc Gly Ser Glu Gly Gln Leu Val Arg Leu Ile 400               405	2993

tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagttaa	3042
Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala	
410	415
aattttagca gaatttgaga ccatttaccc tcatacattt cagattctaa atctcaaaaat	3102
caccatgtct atttcgag gtg aac cta aga aat ctg gaa tgt cac act tta	3154
Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu	
425	430
agc ttt agc act cag ata aac caa tca taacatttag ttgctacttt	3201
Ser Phe Ser Thr Gln Ile Asn Gln Ser	
435	440
ggtagattat ttccctgtttt gaagatgtaa tgttgagttt tttcagtaac acactccat	3261
gttctaacca aatgtttgtt aaaaatcctt tttcttgagt ggaacttcca aatctttgga	3321
tatattggta atgctcattt tttgtccta atttctaaa aatctcgaca cgagttctta	3381
ggtagtcaca taaaggacaa aaaggccga ccagatagtgcgt tggtcagaag	3441
aacgtaaaaa gactgcaaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc	3501
aaatgtctct ctctctttc tcaacggcta tatccatcca cacttattac attataaaaat	3561
taattaaatg caataatgtt acgcattata ttctccaaacg gtccattttc ccgcatttcc	3621
ctaacccttc ctttataacg caaaacagtt tcatacttcta cacttaacac tttaatcctc	3681
tct	3684

Serial No. 10/810,486 Docket No. 690116.401C1

Inventor(s): Mitsuru Furusawa

Express Mail No. EV44955930US "NEW SHEET"

SEQ ID NO:92

3684 nucleotides

DNA

*Arabidopsis thaliana*

CDS

(501)..(557)

(689)..(818)

(1008)..(1114)

(1194)..(1320)

(1469)..(1576)

(1671)..(1786)

(1858)..(1941)

(2040)..(2108)

(2198)..(2269)

(2352)..(2443)

(2545)..(2672)

(2772)..(2873)

(2965)..(3032)

(3122)..(3181)

agcgattcct tagcagaaaag ggcgtccatt tctctggcgt aaaccaaagg agatccttga 60

actgtttcct gcaccattgc tcttaaaacc cttctccggc acgaattctt ccaaccctgc 120

ttcaccacccg gaacattgag acaaaatctc gacggtgacg ctgagggttga aaaaaccaat 180

cgaaccgcag acgtaccagg aaccgaacca tgttatcaacg ccattgaaga agaagaagaa 240

gaagaagggtg aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga 300

*FIG. 20A*

aaaaagagtt aagggtggag tgtctggttc aaccggttta tatccggttc aaattaaacc	360
tcttacagtt aaccgggttt tgtgttttgt tcgattgttc ataaaagaaa gaagactctt	420
gtcgtcgatt agtgccaaag ttgaaagttg aaacctttc tcagaatttt ctgctcagtt	480
cttagtttt ttttcccccc atg gaa atc gac tcc gag aaa att cac gaa agg Met Glu Ile Asp Ser Glu Lys Ile His Glu Arg	533
1                    5                    10	
aag caa tcc gat tac aat tcg ctg gtacgaactc tattacttta tcgacttgta	587
Lys Gln Ser Asp Tyr Asn Ser Leu	
15	
gtgaaagaca aatgtaatca ttcgtgggg tgactgtttc tacttataag tgtacggct	647
agggtttgtt atctgattct gagttttgc aattgaagca g gat gag aga ttc gag Asp Glu Arg Phe Glu	703
20	
ata cag aag gag atg tac aga ggt cag caa tac agt cag att tac ttt Ile Gln Lys Glu Met Tyr Arg Gly Gln Gln Tyr Ser Gln Ile Tyr Phe	751
25                30                35                40	
gct cgt ctt cat ctc atg aga aca ctt ctc tac tct ctt gct cct act Ala Arg Leu His Leu Met Arg Thr Leu Leu Tyr Ser Leu Ala Pro Thr	799
45                50                55	
tgg aaa tct cat ttg cct g gtcagtgc ttgtttctct catatttagc	848
Trp Lys Ser His Leu Pro	
60	
acaacaacga agagcagttt ttgagaattt tctgggtta gatataatta ggtgaaatca	908
gtgattttta gggatttttg ctatcttatg gattacagtt gagaagatt gctagtattg	968
tttaaattat agatctgaat gtgaatttca ttttgcat tg tgt aag gtt ttg Val Cys Lys Val Leu	1021
65	
gga ctt gaa aaa gga aaa gaa tgc ata att gtg gga acc ttg ttc aaa Gly Leu Glu Lys Gly Lys Glu Cys Ile Ile Val Gly Thr Leu Phe Lys	1069
70                75                80	

*FIG. 20B*

cac atg aag ctt aaa cct tgt gtt ctc gat gaa tat tct aaa gag His Met Lys Leu Lys Pro Cys Val Leu Asp Glu Tyr Ser Lys Glu 85                    90                    95	1114
 gttggttttt attaacctct actgttttt tgagctatgt ctatgctgaa tcaatctgag	1174
tatatttaac ataatgcag agg tca gtt act ccg ctt gtt aaa cca cat aac Arg Ser Val Thr Pro Leu Val Lys Pro His Asn 100                    105	1226
 ttt atg cat cct gat gat aat ctg atc ctc gaa gac gag agt ggg aga Phe Met His Pro Asp Asp Asn Leu Ile Leu Glu Asp Glu Ser Gly Arg 110                    115                    120                    125	1274
 gtt aag ctt gct ggt tcc gca ctt tca cct gcg att tat gtg aca g Val Lys Leu Ala Gly Ser Ala Leu Ser Pro Ala Ile Tyr Val Thr 130                    135                    140	1320
 gtattgcaaa tgggttctta ctgttttac tgtatgattt ttcccttctt tacaatgtgg	1380
caaatcttag agattttgat caagcttcc tctctaaaa gatgggttct ttaagaaaat	1440
 taacgttcaa gcctcccgta cattgttag gt gtt gtt gca ctg cat ggg Gly Val Val Val Ala Leu His Gly 145	1491
 aag gaa act aat gct ggt gaa ttc ttt gtt gag gat gta cta gaa gct Lys Glu Thr Asn Ala Gly Glu Phe Phe Val Glu Asp Val Leu Glu Ala 150                    155                    160	1539
 ggt tta cca cct cag att gag cggtt cct atc gat cta c gtaagtctag Gly Leu Pro Pro Gln Ile Glu Arg Pro Ile Asp Leu 165                    170                    175	1586
 ctatgttctc ttccctttgc taacctcatg gctcaatcat ttctataagc aatctctcat	1646
gatacatcca tattgcatct gcag ag gaa gat aaa tat gtc gtg tta ttg Gln Glu Asp Lys Tyr Val Val Leu Leu 180                    185	1696
 tcg ggc ctt tgt att gga agc aaa tcg gct aat ccc ctg cag ttt cag Ser Gly Leu Cys Ile Gly Ser Lys Ser Ala Asn Pro Leu Gln Phe Gln 190                    195                    200	1744

cct ctt gtt gac cat ata act ggg cat ctc gga gat gag gag Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu 205                   210                   215	1786
gttcaaatct cttaacttgc aggttgtca acatatttct ttcctaatt tatactttat gaa caa gaa ggc ctt gca gca cag ata gtt cat gta gta att Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile 220                   225	1846
gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln 230                   235                   240	1896
gtacttataa cttttgtgc tgatatatcc tcagatacag ttccagtaat tatctgccccc atgtatgtct tatgatcttt attgggtgat ctttgtag aac ttg gcc tcg aaa gat Asn Leu Ala Ser Lys Asp 245	2001
caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Mét Leu Ser 250                   255                   260                   265	2105
cag gtcatgttac tggatctacg tgtgtgttat cgatatctat tgagatgaaa Gln	2158
gttcaaactc ctgtttttt ttttgtggat tgtttttag ata gct gca gga gtt Ile Ala Ala Gly Val 270	2212
tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu 275                   280                   285	2260
cct cag cag gtctgcaa at acataagaaa cattcaaa at cccgcatttt Pro Gln Gln 290	2309
gtatcgataa ctctgattca taggccttc tctttgttc ag cct ctg aat aga Pro Leu Asn Arg	2363

tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr 295               300               305               310	2411
aat cct cac tca ttt gct gtc gat aat atc ag gtatgattat tattaatagt Asn Pro His Ser Phe Ala Val Asp Asn Ile Arg 315               320	2463
tgaataacaat ctctctgatt ttacaacgat aaaattctg ggtttatctg actgaaaacc	2523
tcatatgggg gcatttgca g a ttt ctt gga act tct ggt cag aac atc gat Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp 325               330	2575
gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu 335               340               345	2623
aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu 350               355               360	2672
gtaagaattc tccttgcctt gcaagattac tttttgaac taagccata aaaaaatgat	2732
ccttgagtt ctatgggtt ttgattcaact tgcgtagac ag gt tgt tat cct ttc Gly Cys Tyr Pro Phe 365	2785
acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe 370               375               380	2833
gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys 385               390               395	2883
tttacacaga gattagaaat aacattctct tttgtcaaac atcaggctt aactttctt	2943
gggtaaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cggtt atc Gly Ser Glu Gly Gln Leu Val Arg Leu Ile 400               405	2993

tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagttaa	3042
Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala	
410                          415                          420	
 aatttgagca gaatttggaga ccatttaccc tcatacgattt cagattctaa atctcaaaat	3102
caccatgtct atttcgcag gtg aac cta aga aat ctg gaa tgt cac act tta	3154
Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu	
425                          430	
 agc ttt agc act cag ata aac caa tca taacatttag ttgctacttt	3201
Ser Phe Ser Thr Gln Ile Asn Gln Ser	
435                          440	
 ggtagattat ttccgtctt gaagatgtaa tggtagttt tttcgttaac acactcctat	3261
gttctaacca aatgttgtt aaaaatcctt ttttttgagt ggaacttcca aatctttgga	3321
tatattggta atgtcattt ttttgccta attttctaaa aatctcgaca cgagttctta	3381
ggtagtcaca taaaggacaa aaagggccga ccagatagtg tcgtggcgt tggtcagaag	3441
aacgtgaaaa gactgcaaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc	3501
aaatgtctct ctctctttc tcaacggcta tatccatcca cacttattac attataaaat	3561
taattaaatg caataatgtt acgcattata ttctccaacg gtccattttc ccgcatttcc	3621
ctaacccttc ctttataacg caaaacagtt tcatcttcta cacttaacac tttaatcctc	3681
 tct	3684